OIPE

```
                    RAW SEQUENCE LISTING                   DATE: 01/19/2002
                    PATENT APPLICATION:  US/10/037,633     TIME: 11:58:24

                    Input Set : A:\DKGR-SEQS.ST25.txt
                    Output Set: N:\CRF3\01182002\J037633.raw
```

ENTERED

```
      3 <110> APPLICANT: BLABER, MICHAEL
      4       SANLI, GULSAH
      5       BLABER, SACHIKO
      7 <120> TITLE OF INVENTION: SYNTHETIC GENES FOR 2,5-DIKETO-D-GLUCONIC ACID REDUCTASES
      9 <130> FILE REFERENCE: 22201
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/037,633
C--> 11 <141> CURRENT FILING DATE: 2002-01-03
     11 <150> PRIOR APPLICATION NUMBER: US 60/259527
     12 <151> PRIOR FILING DATE: 2001-01-03
     14 <160> NUMBER OF SEQ ID NOS: 6
     16 <170> SOFTWARE: PatentIn version 3.0
     18 <210> SEQ ID NO: 1
     19 <211> LENGTH: 845
     20 <212> TYPE: DNA
     21 <213> ORGANISM: Corynebacterium species
     23 <220> FEATURE:
     24 <221> NAME/KEY: misc_feature
     25 <223> OTHER INFORMATION: "n" positions designate restriction endonuclease recognition
site
     29 <400> SEQUENCE: 1
W--> 30 nnnatgacag ttcccagcat cgtgctcaac gacggcaatt ccattcccca gctcgggtac      60
     32 ggcgtcttca aggtgccgcc ggcggacacc cagcgcgccg tcgaggaagc gctcgaagtc     120
     34 ggctaccggc acatcgacac cgcggcgatc tacggaaacg aagaaggcgt cggcgccgcg     180
     36 atcgcggcga gcggcatcgc gcgcgacgac ctgttcatca cgacgaagct ctggaacgat     240
     38 cgccacgacg gcgatgagcc cgctgcagcg atcgccgaga gcctcgcgaa gctggcactc     300
     40 gatcaggtcg acctgtacct cgtgcactgg ccgacgcccg ccgccgacaa ctacgtgcac     360
     42 gcgtgggaga agatgatcga gcttcgcgca gccggtctca cccgcagcat cggcgtctcg     420
     44 aaccacctcg tgccgcacct cgagcgcatc gtcgccgcca ccggcgtcgt gccggcggtg     480
     46 aaccagatcg agctgcaccc cgcctaccag cagcgcgaga tcaccgactg ggccgccgcc     540
     48 cacgacgtga agatcgaatc gtgggggccg ctcggtcagg gcaagtacga cctcttcggc     600
     50 gccgagcccg tcactgcggc [illegible] [illegible] [illegible] ggccgtgctc     660
     52 cgttggcacc tgcagaaggg tttcgtgatc ttcccgaagt cggtccgccg cgagcgcctc     720
     54 [illegible] [illegible] [illegible] [illegible] ccgagatcgc cgcgatcgac     780
     56 gcgatggatc cgggcgacgg ttcgggtcgc gtgagcgcac accccgatga ggtcgactga     [illegible]
W--> 58 nnnnn                                                                845
     61 <210> SEQ ID NO: 2
     62 <211> LENGTH: 845
     63 <212> TYPE: DNA
     64 <213> ORGANISM: Corynebacterium species
     66 <400> SEQUENCE: 2
     67 catatgaccg ttccgtctat cgttctgaac gacggtaact ctatcccgca gctgggttac      60
     69 ggtgttttca aagttccgcc ggctgacacc cagcgtgctg ttgaagaagc tctggaagtt     120
     71 ggttaccgtc acatcgacac cgctgctatc tacggcaacg aagaaggtgt tggtgctgct     180
     73 atcgctgctt ctggtatcgc tcgtgacgac ctgttcatca ccaccaaact gtggaacgac     240
```

```
                    RAW SEQUENCE LISTING                   DATE: 01/19/2002
                    PATENT APPLICATION:  US/10/037,633     TIME: 11:58:24

                    Input Set : A:\DKGR-SEQS.ST25.txt
                    Output Set: N:\CRF3\01182002\J037633.raw

      75 cgccacgacg gtgacgaacc ggctgctgct atcgctgaat ctctggctaa actggctctg     300
      77 gatcaggttg acctgtacct ggttcactgg ccgaccccgg ctgctgacaa ctacgttcac     360
      79 gcttgggaaa aaatgatcga actgcgtgct gctggtctga cccgttctat cggtgtttct     420
      81 aaccacctgg ttccgcacct ggaacgtatc gttgctgcta ccggtgttgt tccggctgtt     480
      83 aaccagatcg aactgcaccc ggcttaccag cagcgtgaaa tcaccgactg ggctgctgct     540
      85 cacgacgtta aaatcgaatc ttggggtccg ctgggtcagg gtaaatacga cctgttcggt     600
      87 gctgaaccgg taaccgctgc tgctgctgct cacggtaaaa ccccggctca ggctgttctg     660
      89 cgttggcacc tgcagaaagg tttcgttgtt ttcccgaaat ctgttcgtcg tgaacgtctg     720
      91 gaagaaaacc tggacgtttt cgacttcgac ctgaccgaca ccgaaatcgc tgctatcgac     780
      93 gctatggatc cgggcgacgg ttctggtcgt gtttctgctc acccggacga agttgactga     840
      95 agctt                                                                 845
      98 <210> SEQ ID NO: 3
      99 <211> LENGTH: 843
     100 <212> TYPE: DNA
     101 <213> ORGANISM: Corynebacterium species
     103 <220> FEATURE:
     104 <221> NAME/KEY: misc_feature
     105 <223> OTHER INFORMATION: "n" positions at both ends of sequence represent restriction
endo
     106       nuclease recognition sites; "n" positions at residues 49-51, and
     107       55-57 represent areas of disagreement in the published sequence f
     108       or wild type DKGR-B between Sonoyama and Powers, however, both pu
W--> 109       blished sequences encode the same amino acid
     112 <400> SEQUENCE: 3
W--> 113 nnnatgccga acatccccac catcagcctc aacgacggac gccccttcnn ngagnnnggg      60
     115 ctcggcacgt acaacctgcg cggcgacgag gggtcgcgg ccatggtcgc cgcgatcgac     120
     117 tcgggctacc gcctgctcga cacggcggtg aactacgaga acgagagcga ggtcggccga     180
     119 gcggtgcgcg cgagcagcgt cgatcgcgac gagctcatcg tggcgagcaa gatcccgggc     240
     121 cgccagcacg ggcgcgccga ggcggtcgac agcatccgcg gatcgctcga ccggctgggg     300
     123 ctcgacgtga tcgacctgca gctgatccac tggccgaacc ccagcgtggg ccggtggctc     360
     125 gacacctggc gcggcatgat cgacgcgcgc gaggcgggcc tggtccgctc gatcggcgtc     420
     127 tcgaacttca ccgagccgat gctgaagacc ctcatcgacg agaccgggt cacacccgcg      480
     129 gtcaaccagg tcgagctcca cccgtacttc cgccaggcgg cgctgcgcgc gttccacgac     540
     131 gagcacggca tccgcaccga gagctggagc ccgctcgccc ggcgcagcga gctgctcacc     600
     133 gagcagctgc tgcaggagct ggcggtcgtc tacggagtga cgccgacgca ggtggtgctg     660
     135 cggtggcacg tgcagctcgg cagcaccccg atccccaagt ccgccgaccc cgatcgccag     720
     137 cgcgagaacg ccgatgtgtt cggcttcgcc ctcaccgccg accaggtcga tgcgatctcg     780
W--> 139 ggcctcgagc gcgggcggct ctgggacggc gaccccgaca cgcacgaaga gatgtagnnn     840
W--> 141 nnn                                                                   843
     144 <210> SEQ ID NO: 4
     145 <211> LENGTH: 843
     146 <212> TYPE: DNA
     147 <213> ORGANISM: Corynebacterium species
     149 <400> SEQUENCE: 4
     150 catatgccga acatcccgac catctctctg aacgacggtc gtccgttccc ggaactgggt      60
     152 ctgggtacct acaacctgcg tggtgacgaa ggtattgctg ctatggttgc tgctatcgac    120
     154 tctggttacc gtctgctgga caccgctgtt aactacgaaa acgaatctga agttggtcgt    180
     156 gctgttcgtg cttcttctgt tgaccgtgac gaactgatcg ttgcttctaa aatcccgggt    240
     158 cgtcagcacg gtcgtgctga agctgttgac tctatccgtg gttctctgga ccgtctgggt    300
     160 ctggacgtta tcgacctgca gctgatccac tggccgaacc cgtctgttgg tcgttggctg    360
```

```
RAW SEQUENCE LISTING                          DATE: 01/19/2002
PATENT APPLICATION:  US/10/037,633            TIME: 11:58:24

Input Set : A:\DKGR-SEQS.ST25.txt
Output Set: N:\CRF3\01182002\J037633.raw

162 gacacctggc gtggtatgat cgacgctcgt gaagctggtc tggttcgttc tatcggtgtc    420
164 tctaacttca ccgaaccgat gctgaaaacc ctgatcgacg aaaccggtgt taccccggct    480
166 gttaaccagg ttgaactgca cccgtacttc ccgcaggctg ctctgcgtgc tttccacgac    540
168 gaacacggta tccgtaccga atcttggtct ccgctggctc gtcgttctga actgctgacc    600
170 gaacagctgc tgcaggaact ggctgttgtt tacggtgtta ccccgaccca ggttgttctg    660
172 cgttggcacg ttcagctggg ttctaccccg atcccgaaat ctgctgaccc ggaccgtcag    720
174 cgtgaaaacg cagacgtttt cggtttcgct ctgaccgctg accaggttga cgctatctct    780
176 ggtctggaac gtggtcgtct gtgggacggt gacccggaca cccacgaaga aatgtagaag    840
178 ctt                                                                  843
181 <210> SEQ ID NO: 5
182 <211> LENGTH: 277
183 <212> TYPE: PRT
184 <213> ORGANISM: Corynebacterium species
186 <400> SEQUENCE: 5
188 Met Thr Val Pro Ser Ile Val Leu Asn Asp Gly Asn Ser Ile Pro Gln
189 1               5                   10                  15
191 Leu Gly Tyr Gly Val Phe Lys Val Pro Pro Ala Asp Thr Gln Arg Ala
192             20                  25                  30
194 Val Glu Glu Ala Leu Glu Val Gly Tyr Arg His Ile Asp Thr Ala Ala
195         35                  40                  45
197 Ile Tyr Gly Asn Glu Glu Gly Val Gly Ala Ala Ile Ala Ala Ser Gly
198     50                  55                  60
200 Ile Ala Arg Asp Asp Leu Phe Ile Thr Thr Lys Leu Trp Asn Asp Arg
201 65                  70                  75                  80
203 His Asp Gly Asp Glu Pro Ala Ala Ala Ile Ala Glu Ser Leu Ala Lys
204                 85                  90                  95
206 Leu Ala Leu Asp Gln Val Asp Leu Tyr Leu Val His Trp Pro Thr Pro
207             100                 105                 110
209 Ala Ala Asp Asn Tyr Val His Ala Trp Glu Lys Met Ile Glu Leu Arg
210         115                 120                 125
212 Ala Ala Gly Leu Thr Arg Ser Ile Gly Val Ser Asn His Leu Val Pro
213     130                 135                 140
215 His Leu Glu Arg Ile Val Ala Ala Thr Gly Val Val Pro Ala Val Asn
216 145                 150                 155                 160
218 Gln Glu Leu His Pro Ala Tyr Gln Gln Arg Glu Ile Thr Asp Trp Ala
219                 165                 170                 175
221 Ala Ala His Asp Val Lys Ile Glu Ser Trp Gly Pro Leu Gly Gln Gly
222             180                 185                 190
224 Lys Tyr Asp [illegible] Phe Gly Ala Gln Pro Val Thr Ala Ala Ala Ala Ala
225         195                 200                 205
227 [illegible] [illegible] [illegible] Thr Pro Ala Gln Ala Val Leu Arg Trp His Leu Gln Lys
228     210                 215                 220
230 Gly Phe Val Val Phe Pro Lys Ser Val Arg Arg Glu Arg Leu Glu Glu
231 225                 230                 235                 240
233 Asp Leu Asp Val Phe Asp Phe Asp Leu Thr Asp Thr Glu Ile Ala Ala
234                 245                 250                 255
236 Ile Asp Ala Met Asp Pro Gly Asp Gly Ser Gly Arg Val Ser Ala His
237             260                 265                 270
239 Pro Asp Glu Val Asp
```

```
            275
<210> SEQ ID NO: 6
<211> LENGTH: 277
<212> TYPE: PRT
<213> ORGANISM: Corynebacterium species
<400> SEQUENCE: 6
Met Pro Asn Ile Pro Thr Ile Ser Leu Asn Asp Gly Arg Pro Phe Pro
1               5                   10                  15
Glu Leu Gly Leu Gly Thr Tyr Asn Leu Arg Gly Asp Glu Gly Val Ala
            20                  25                  30
Ala Met Val Ala Ala Ile Asp Ser Gly Tyr Arg Leu Leu Asp Thr Ala
        35                  40                  45
Val Asn Tyr Glu Asn Glu Ser Glu Val Gly Arg Ala Val Arg Ala Ser
    50                  55                  60
Ser Val Asp Arg Asp Glu Leu Ile Val Ala Ser Lys Ile Pro Gly Arg
65                  70                  75                  80
Gln His Gly Arg Ala Glu Ala Val Asp Ser Ile Arg Gly Ser Leu Asp
                85                  90                  95
Arg Leu Gly Leu Asp Val Ile Asp Leu Gln Leu Ile His Trp Pro Asn
            100                 105                 110
Pro Ser Val Gly Arg Trp Leu Asp Thr Trp Arg Gly Met Ile Asp Ala
        115                 120                 125
Arg Glu Ala Gly Leu Val Arg Ser Ile Gly Val Ser Asn Phe Thr Glu
    130                 135                 140
Pro Met Leu Lys Thr Leu Ile Asp Glu Thr Gly Val Thr Pro Ala Val
145                 150                 155                 160
Asn Gln Val Glu Leu His Pro Tyr Phe Pro Gln Ala Ala Leu Arg Ala
                165                 170                 175
Phe His Asp Glu His Gly Ile Arg Thr Glu Ser Trp Ser Pro Leu Ala
            180                 185                 190
Arg Arg Ser Glu Leu Leu Thr Glu Gln Leu Leu Gln Glu Leu Ala Val
        195                 200                 205
Val Tyr Gly Val Thr Pro Thr Gln Val Val Leu Arg Trp His Val Gln
    210                 215                 220
Leu Gly Ser Thr Pro Ile Pro Lys Ser Ala Asp Pro Asp Arg Gln Arg
225                 230                 235                 240
Glu Asn Ala Asp Val Phe Gly Phe Ala Leu Thr Ala Asp Gln Val Asp
                245                 250                 255
Ala Ile Ser Gly [illegible] [illegible] [illegible] Gly Arg Leu Trp Asp Gly Asp Pro Asp
            260                 265                 2
[illegible]
            275
```

```
                    VERIFICATION SUMMARY                    DATE: 01/19/2002
                    PATENT APPLICATION:  US/10/037,633      TIME: 11:58:25

                    Input Set : A:\DKGR-SEQS.ST25.txt
                    Output Set: N:\CRF3\01182002\J037633.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:30 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:30 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:58 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:109 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:113 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:139 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:141 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
```